

Blast 2 Sequences

Exhibit 3

NCBI	Entrez	BLAST 2 sequences	BLAST	Example	Help
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BLAST 2 SEQUENCES

This tool produces the alignment of two given sequences using BLAST engine for local alignment. The stand-alone executable for blasting two sequences (bl2seq) can be retrieved from NCBI ftp site.
Reference: Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250

Program Matrix

Parameters used in BLASTN program only:

Reward for a match: Penalty for a mismatch: ☐ Use Mega BLAST Strand option Open gap and extension gap penalties
gap x_dropoff expect word size Filter ☒Sequence 1 Enter accession or GI or download from file Browse...
or sequence in FASTA format from: to: Sequence 2 Enter accession or GI or download from file Browse...
or sequence in FASTA format from: to:

cgaccaagtctagagcgcttcggt

Comments and suggestions to: blast-help@ncbi.nlm.nih.gov
Credits to: [Tatiana Tatusov](#) and [Tom Madden](#)

**Blast 2 Sequences results**

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.2 [Dec-14-2001]Match: Mismatch: gap open: gap extension: x_dropoff: expect: wordsize: Filter ☒ Align

Sequence 1 gi 13017635 Homo sapiens endothelial differentiation, sphingolipid G-protein-coupled receptor, 1 (EDG1), mRNA Length 2753

Sequence 2 lcl|s:q_2 Length 25

No significant similarity was found